

MARKER ORDER:

D12S100 (TEL)

D12S1050

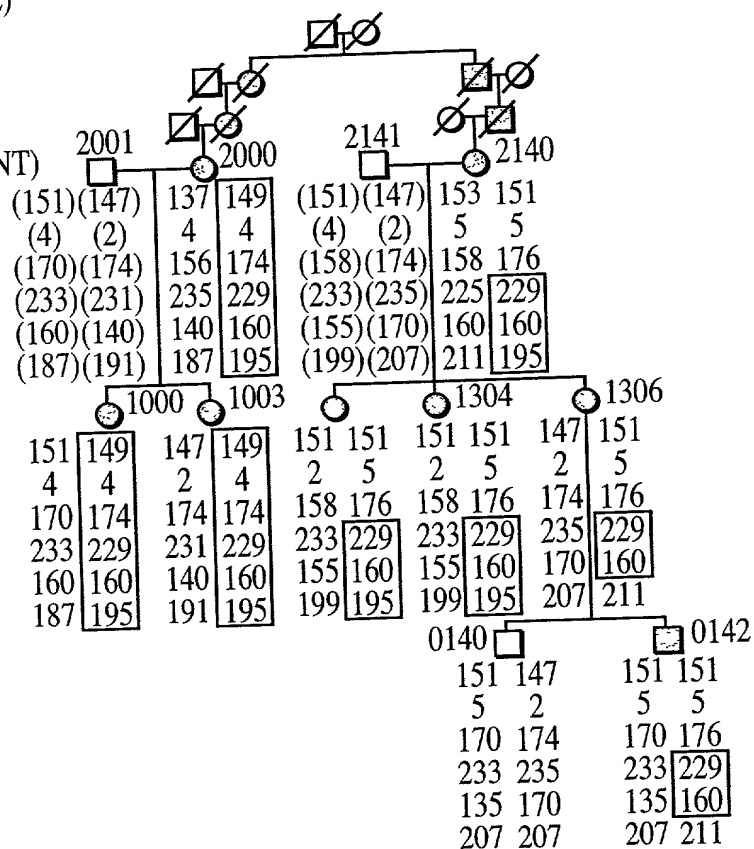
D12S1685

D12S1624

CD4

D12S397 (CENT)

FAMILY 1406



FAMILY 1478

MARKER ORDER:

D12S100 (TEL)

D12S1050

D12S1685

D12S1624

D12S1594

D12S397 (CENT)

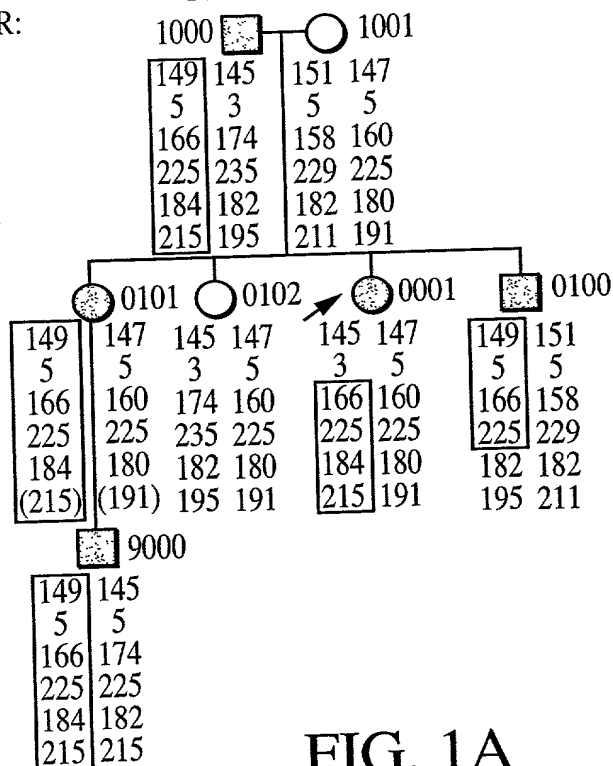


FIG. 1A

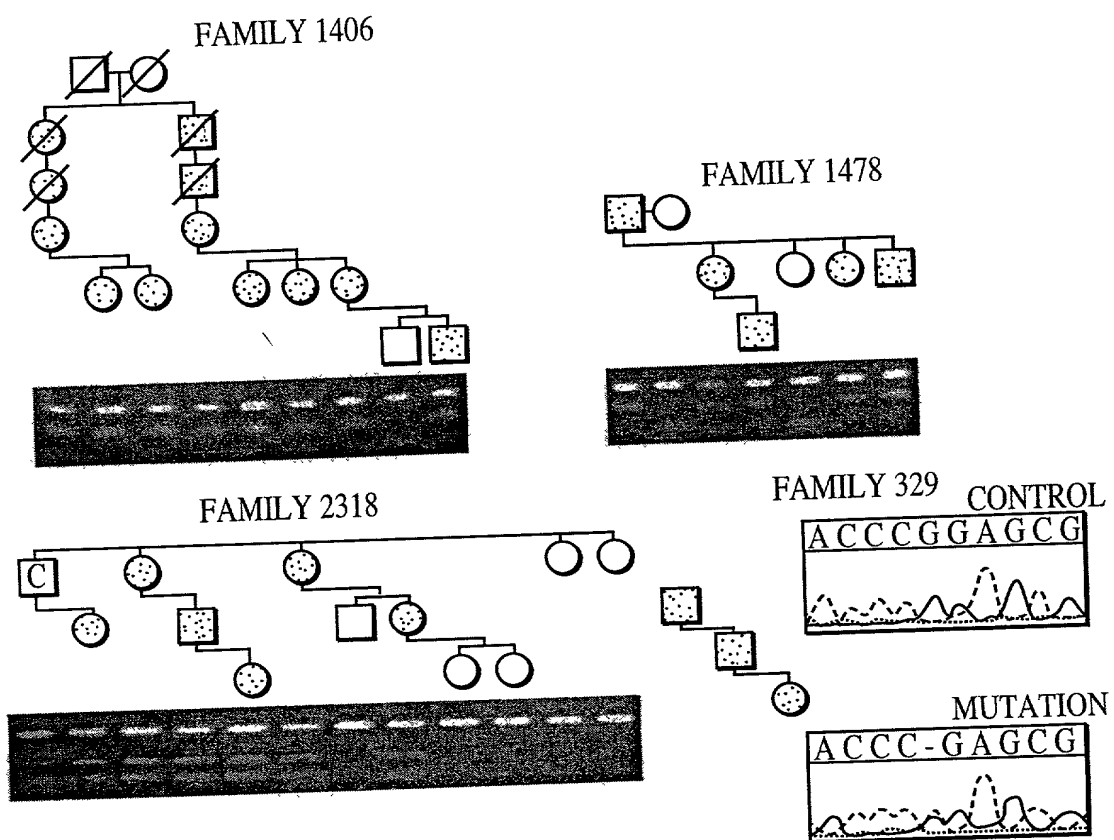


FIG. 1B

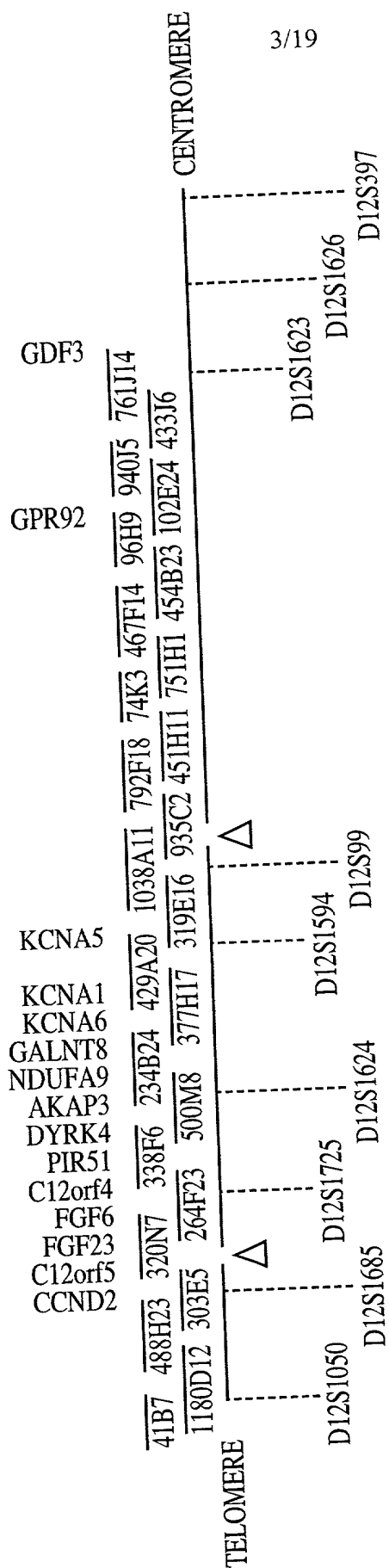


FIG. 2

T00T'00" 8E6T0660

FGF12	LKG. IVT.	YFLQHPDGTIDG	TKDENS	YTLFNLIPVGLR.	114
FGF14	LKG. IVT.	YFLQHPDGDALD	GTKDDSTN	STLFLNIPVGLR.	112
FGF13	LKG. IVT.	YHLQLQADGTID	GTKDEDS	YTLFNLIPVGLR.	110
FGF11	LKG. IVT.	FYLQANPDGSIQ	GTPEDTSS	FTHFNLI	112
FGF16	LKG. ILRRRQLYCR	TG.	FHLEIFP	NGTVHGRHDS	102
FGF9	LKG. ILRRRQLYCR	TG.	FHLEIFP	NGTIQGRKDH	103
FGF10	LQG. DWRWRKLF	FTK.	YFLKIEK	NGKVS	119
FGF7	MEGGDIRVRR	LFCTRQ.	WYLRID	KRGKVG	106
FGF3	LGGAPRR. RKLY	CATK.	YHLQLH	PSGRV	84
FGF1	PPGNYKKPKLL	YCSNG.	GHFLRI	LPDGT	67
FGF2	PPGHFKDPKRL	YCKNG.	GFFLRI	HPDGR	125
FGF4	LLGIKRL. RRL	YCNVGI.	GFHLQ	ALPDGR	124
FGF6	LVGIKRQ. RRL	YCNVGI.	GFHLQ	VLDPDGR	126
FGF5	SPS. GRRTG	SLYCRVG.	IGFHLQ	IYPDG	129
FGF18	VSRKQLRLYQ	LYSRTS.	GKHIQ	VLG. RR	95
FGF8	LSRRLIRTYQ	LYSRTS.	GKHVQ	VLANKR	95
FGF17	LSRRQIREYQ	LYSRTS.	GKHVQ	VTG. RR	95
FGF15	GWGKI	TRLQYLYSAGPY. V	SNCF	FLRIRSDG	95
FGF19	GWGDP	IRLRHLYTSGPHGL	SSCF	FLRIRADG	88
FGF21	QFGGQVRQRY	LYTDDAQQT. E	AHLEI	REDGTV	89
FGF23	SWG.	LIHLYTATARN. S.	YHLQ	IHKNGH	81

1—1—
 —2—
 —3—
 —4—

FIG. 3A

T00T 20" BE5T0560

FGF12	VVAIQGVKASLYVAMNGEGYLYSSDV.FTPECKFKESVFENYYVVIYSSTLY...	164
FGF14	VVAIQGVKTGLYIAMNGEGYLYPSEL.FTPECKFKESVFENYYVVIYSSTLY...	162
FGF13	VVAIQGVQTKLYLAMNSEGYLYTSEL.FTPECKFKESVFENYYVVIYSSTLY...	160
FGF11	VVTIQSAKLGHYMAMNAEGLLYSSPH.FTAECRFKECVFENYYVLYASALY...	162
FGF16	LISIRGVD SGLYLGMNERGELYGSKK.LTREC VFREQFEENWYNTYASTLY...	152
FGF9	LV SIRGVD SGLYLGMNEK GELYGSEK.LTQEC VFREQFEENWYNTYSSNLY...	153
FGF10	VVAVKAINSNYYLAMNKKGLYGSKE.FNNDCKLKERIEENG YNTYASFNW...	169
FGF7	IVAIKGVES E FYLAMNKEGKLYAKKE.CNEDCNFKELILENH YNTYASAKW...	156
FGF3	IVAIRGLFSGRYLAMNKRGRLYASEH.YSAECE FVERIHELGYNTYASRLYRTV	137
FGF1	EVIKSTETGQYLAMDTDGLLYGSQT.PNEEC LFLERLEENHYNTYISKKH...	117
FGF2	VVSIKGVCANRYLAMKEDGRLLASKC.VTDEC FFFERLESNNYNTYRSRKY...	175
FGF4	VVSIFGVASRFFVAMSSKGKLYGSPF.FTDEC TFKEILLPNNYNAYESYKY...	174
FGF6	VVSLFGVRSALFVAMNSKGRLYATPS.FQEECKFRETL LPNNYNAYESDLY...	176
FGF5	IVGIRGVFSNKKFLAMSKKGLHASAK.FTDDCKFRERFQENS YNTYASAIHRTE	182
FGF18	QVRIKGKET E FYLCMNRKGLVGKPDGTSKECVFIEKVLENNY TALMSAKY...	146
FGF8	RVRVRGAETGLYICMNRKGLI AKSNGKGD CVFTEIVLENNY TALQNAKY...	146
FGF17	RVRIKGAESEKYICMNRKGLIGKPSGKSKDCVFTEIVLENNY TAFQNAH...	146
FGF15	TIAIKDVSSVRYLCMSADGKIYGLIRYSEEDCTFREEMDC LGYNQYRSMKH...	146
FGF19	TVAIKGVHSVRYLCMGADGKMQLLYSEEDCAFE EIRPDGYNVYRSEKH...	139
FGF21	VIQILGVKTSRFLCQRPD GALYGS LHFDP EACSFRELLLEDGYNVYQSEAH...	140
FGF23	FVVI TGVM SRRYLCMDFRGNIFGSHYFDPENC RFQHQTLENGYDVYHSPQYHFL	135

FIG. 3B

FGF12RQ	QES	GRA	WFL	GLN	KEG	QIM	KGN	..	RVK	KTK	PSS	H	F	V	P	K	P	I	E	V	C	M	Y	208																				
FGF14RQ	QES	GRA	WFL	GLN	KEG	QAM	KGN	..	RVK	KTK	PAA	H	F	L	P	K	P	L	E	V	A	M	Y	206																				
FGF13RQ	QOS	GRG	WYL	GLN	KEG	EIM	KGN	..	HVK	KNK	PAA	H	F	L	P	K	P	L	K	V	A	M	Y	204																				
FGF11RQ	RRS	GRA	WYL	GLD	KEG	QVM	KGN	..	RVK	KTK	AAA	H	F	L	P	K	L	L	E	V	A	M	Y	206																				
FGF16KH	SDS	ERQ	YYV	ALN	KDG	SPR	EGY	..	RTK	RHQ	KFT	H	F	L	P	R	P	V	D	P	S	K	L	196																				
FGF9KH	VDT	GRR	YYV	ALN	KDG	TPR	EGT	..	RTK	RHQ	KFT	H	F	L	P	R	P	V	D	P	D	K	V	197																				
FGF10QH	NRQ	Q	MYV	ALN	GKG	APR	RRQ	..	KTR	RKN	TS	A	H	F	L	P	M	V	H	S	~	~	~	208																				
FGF7TH	NGG	EMF	VAL	NQK	GIP	VRG	K..	..	KTK	KEQ	KTA	H	F	L	P	M	A	I	T	~	~	~	~	194																				
FGF3	SS	TPG	ARR	Q	PSA	ERL	WYV	SVN	GKGR	PRRG	F..	KTR	RTQ	KSS	L	F	L	P	R	V	L	D	H	R	D	188																			
FGF1A	EKN	WFV	GLK	KN	GSC	KRG	P..	..	RTH	YGQ	KAIL	F	L	P	L	P	V	S	S	D	~	~	~	155																				
FGF2T	SWY	VAL	KRT	GQY	KLG	S..	KTG	PGQ	KAIL	F	L	P	M	S	A	K	S	~	~	~	~	210																				
FGF4P	G	M	F	I	A	L	S	KNG	TKK	GN..	RVS	PTM	KV	T	H	F	L	P	R	L	~	~	~	~	206																			
FGF6Q	G	T	Y	I	A	L	S	KYGR	VKRG	S..	KVS	PIM	T	V	T	H	F	L	P	R	I	~	~	~	208																			
FGF5G	R	E	W	Y	VAL	NKRG	KAK	RGC	S	PRV	KPQ	HIS	T	H	F	L	P	R	F	K	Q	S	E	Q	P	225																		
FGF18S	G	W	Y	V	G	FTK	KGR	PRK	GP..	KTR	ENQ	QD	VH	F	M	K	R	Y	P	K	G	Q	P	..	183																			
FGF8E	G	W	Y	M	A	FTR	KGR	PRK	GS..	KTR	QH	QRE	VH	F	M	K	R	L	P	R	G	H	T	..	184																			
FGF17E	G	W	F	M	A	FTR	QGR	PRQ	AS..	RSR	Q	QRE	AH	F	I	K	R	L	Y	Q	G	Q	L	P	184																			
FGF15H	L	H	I	F	I	Q	A	K	P	R	E	Q	L..	..	Q	D	K	P	S	N	F	I	P	V	F	H	R	S	F	F	E	179												
FGF19R	L	P	V	S	L	S	S	A	K	Q	R	Q	L	Y..	..	K	N	R	G	F	L	P	L	S	H	F	L	P	M	L	P	M	V	P	E	175								
FGF21G	L	P	L	H	L	P	G	N	K	S	P	H	R	D	P..	..	A	P	R	..	G	P	A	R	F	L	P	L	P	G	L	P	P	A	L	174								
FGF23	V	S	LG	R	A	K	R	A	F	L	P	G	M	N	P	P	Y	S	Q	F	L	S	R	R	N	E	I	P	L	I	H	F	N	T	P	I	P	R	R	H	T	R	..	179

FIG. 3C

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FIG. 4A



FIG. 4B

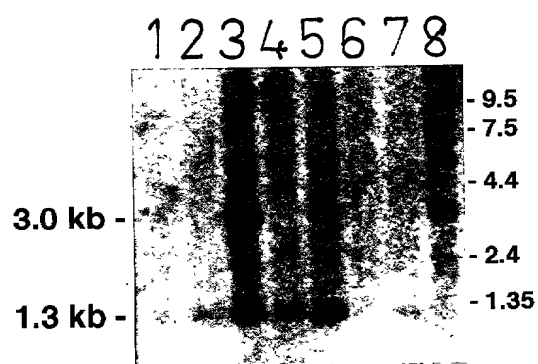


Figure 5A

CGGCAAAAAGGAGGGAATCCAGTCTAGGATCCTCACACCAGCTACTTGC
 AAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTCCCGACA
 GGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGA
 TGTTGGGGGCCCCGCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTG
 CAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGC
 TCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACA
 GCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCA
 TCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT
 GTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCA
 GAGGCAACATTTTTTGGATCACACTATTTTCGACCCGGAGAACTGCAGGTT
 CCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAG
 TATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAG
 GCATGAACCCACCCCGTACTCCCAGTTCTGTCCCGGAGGAACGAGAT
 CCCCCTAATTCACTTCAACACCCCCCATAACCACGGCGGCACACCCGGAGC
 GCCGAGGACGACTCGGAGCGGGACCCCTGAACGTGCTGAAGCCCCGGG
 CCCGGATGACCCCGGCCCGGCCTCCTGTTTACAGGAGCTCCCGAGCGC
 CGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC
 GGTCGAGTGAACACGCACGCTGGGGGAACGGGCCCCGGAAGGCTGCCGCC
 CCTTCGCCAAGTTTATCTAGGGTCGCTGGAAGGGCACCTCTTTAACCC
 ATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTT
 CGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCT
 GGGGTCCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAA
 GTCATGGGGTTTACCGCCTTCTCTACTCCATATAGAACACCTTTCCCA
 ATAGGAAACCCCAACAGGTAACTAGAAATTTCCCCTTCATGAAGGTAG
 AGAGAAGGGTCTCTCCCAACATATTTCTCTTCTTGTGCCTCTCCTCT
 TTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 GCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAAT
 CGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGC
 CCCGATCCCCTGGCATTGAGTGTGCAAACCTTGACATTAACAGCTGA
 ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTCCTTG
 AGCATCTCTGGGGAAGAGCTGTCAAAGACTGGTGGTAGGCTGGTGAAA
 ACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAAT
 AGAAAACCTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT

Figure 5B

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MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN
SYHLQIHKNGHVGDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDF
RGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLP
GMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPR
ARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCR
PFAKFI

09901938.074001

Figure 6A

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AGCCTGTCTGGGAGTGTCTAGATTTCAAACCTCAGCATTAGCCACTCAGTG
CTGTGCAATGCTAGGGACCTGCCTTAGACTCCTGGTGGGCGTGCTCTGC
ACTGTCTGCAGCTTGGGCACTGCTAGAGCCTATCCGGACACTTCCCCAT
TGCTTGGCTCCAACTGGGGAAGCCTGACCCACCTGTACACGGCTACAGC
CAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCATGTAGATGGC
ACCCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACG
CCGGCTCTGTGGTGATAACAGGAGCCATGACTCGAAGGTTCTTTGTAT
GGATCTCCACGGCAACATTTTTGGATCGCTTCACTTCAGCCCAGAGAAT
TGCAAGTTCGCGCCAGTGGACGCTGGAGAATGGCTATGACGTCTACTTGT
CGCAGAAGCATCACTACCTGGTGAGCCTGGGCGCGCCAAGCGCATCTT
CCAGCCGGGCACCAACCCGCCGCCCTTCTCCCAGTTCCTGGCTCGCAGG
AACGAGGTCCCGCTGCTGCATTTCTACACTGTTTCGCCCACGGCGCCACA
CGCGCAGCGCCGAGGACCCACCGGAGCGCGACCCACTGAACGTGCTCAA
GCCGCGGCCCCGCGCCACGCCTGTGCCTGTATCCTGCTCTCGCGAGCTG
CCGAGCGCAGAGGAAGGTGGCCCCGCGAGCCAGCGATCCTCTGGGGGTGC
TGCGCAGAGGCCGTGGAGATGCTCGCGGGGGCGCGGGAGGCGCGGATAG
GTGTCGCCCCCTTTCCCAGGTTTCGTCTAGGTCCCCAGGCCAGGCTGCGTC
CGCCTCCATCCTCCAGTCGGTTCAGCCACGCTAGAGGAAGGACTAGGGT
ACCTCGAGGATGTCTGCTTCTCTCCCTTCCCTATGGGCCTGAGAGTCAC
CTGCGAGGTTCCAGCCAGGCACCGCTATTCAGAATTAAGAGCCAACGGT
GGGAGGCTGGAGAGGTGGCGCAGACAGTTCTCAGCACCCACAAATACCT
GTAATTCTAGCTCCAGGGGAATCTGTACTCACACACACACATCCACA
CACACACACACACACATACATGTAATTTTAAATGTTAATCTGATTTAAA
GACCCCAACAGGTAAACTAGACACGAAGCTCTTTTTATTTTATTTTACT
AACAGGTAAACCAGACACTTGGCCTTTATTAGCCGGGTCTCTTGCCTAG
CATTTTAATCGATCAGTTAGCACGAGGAAAGAGTTCACGCCTTGAACAC
AGGGAAGAGGCCATCTCTGCAGCTTCTAGTTACTATTCTGGGATTACAG
GGTGTTTGAGTTTGAGCACCTTGACCTTAATGTCTTCACTAGGCAAGTC
GAAGAAAGACGCGCATTTCTTCTCTTTGGGAAGAGCTTTGGATTGGCGG
GAGGCTGACAAGGACACCTAAACCGAACACATTTAGAGTTTCAACCTCC
CTGAGGAATGATTCGCCAATGATTCTGTGATAGGACCAGTCAGTAGCTT
TTGAATTTGCCCTGGCTCAGCAAAGTCTACCTTGCTAGGG

Figure 6B

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MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYTATART
SYHLQIHRDGHVDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDL
HGNI FGSLHFSPENCKFRQWTLNGYDVYLSQKHHYLVSLGRAKRI FQP
GTNPPPF SQFLARRNEVPLLHFYTVRPRRHTRSAEDPPERDPLNVLKPR
PRATPVVPVSCSRELPSAEEGGPAASDPLGVLRGRGDARGGAGGADRCR
PFPRFV

0901938.071004

PROJON

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FIG.8A

1 2 3 4 5 6 7 8 9 10



- 3 kb

- 1.3 kb

FIG.8B

- +



- 32 kDa

Figure 9

PREDICTED SIGNAL SEQUENCE
MLGARLRLLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN
 SY
 HLQIHKNQGHVDGAPHQTIYSALMIRSEDAGFVVTGVMSRRYLCMDFRGNI
 FGSHYFDPENC RFQHQTLENGYDVYHSPQYHFLVSLGKAKRAFLPGMNP
 PP
 YSQFLSRNEIPLIHFNTPIPR**R**_{HT}SAEDDSE_{RD}PLNVLPKPRARMT
 PA
 PASCSQELPSAEDNSPMA SDPLGVVRGGRVNT HAGGTGPEGCRPF
 AKFI
 176 179
 PREDICTED PROTEASE CLEAVAGE SITE

FIG.10A

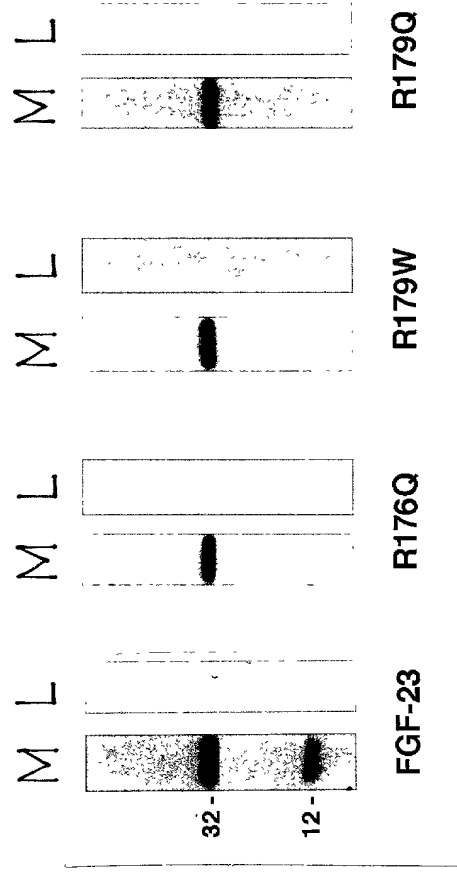


Figure 10B

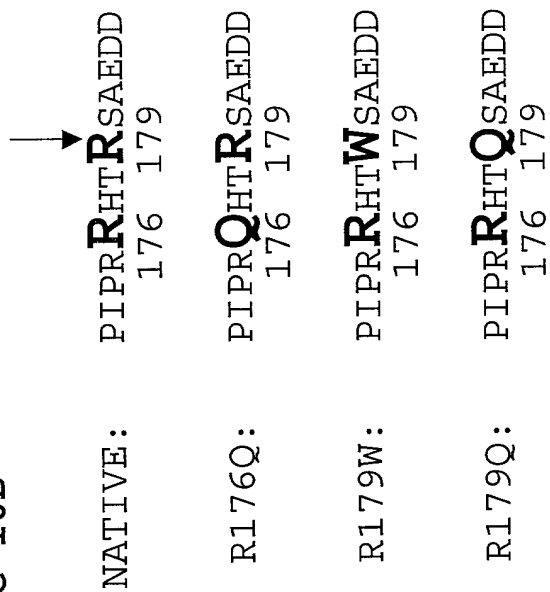


FIG.11A

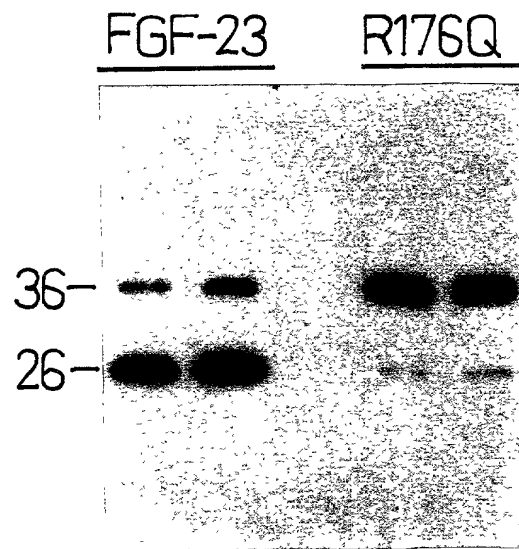


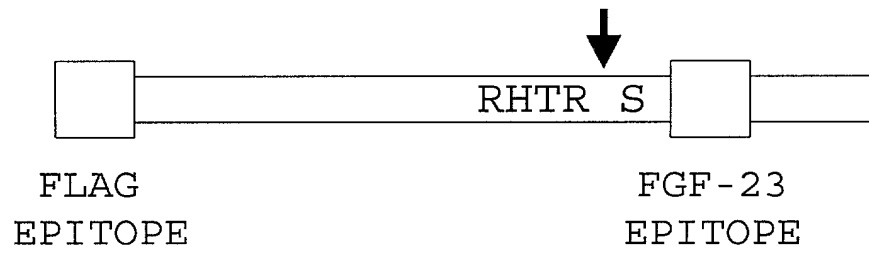
FIG. 11B

FIG. 12A

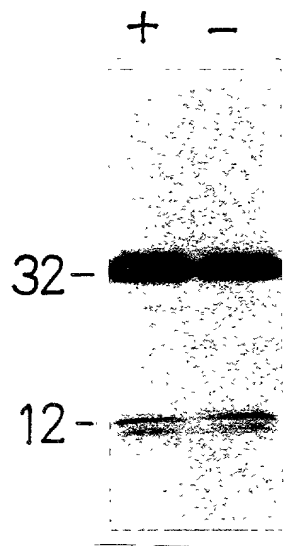


FIG. 12B

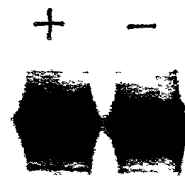


FIG. 13

